SEQUENCE LISTING

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      ZHANG, ZHIPING

<120> ADH7 NUCLEOTIDES

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<140> 10/619,545
<141> 2003-07-16

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<151> 1998-06-26

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accacatcaa gtctttgcag aatgaagtag agcattaaga agtagagatg tacacacgca 180

tctctaaaat cagccatgcc taggcaaagc agcttgcact taaacaccca atacattttt 240

catgattgtg ttgaagtgaa gtaacctaac ccgtttttat atccttcaaa ataaggtgga 300

taggaatgct ttcagcccctt ttcaatagct ttgattatct tgttttttgtt agatccctcc 360

tcttggtttg atcatagtag ttactgtatt tcttttttata agctggtctg caaagggtag 420

ggcttgcaga ccattgcaaa gttgtgacgg ctgtgagtca tattgctgaa ggtggaactc 480

tgaagccaga ctatctatgt gaaggcacaa gctgctgtta tatacaacag agtgaactga 540

gcatcagtca gaaaaagtct atgtttgcag aaatacagat ccaagacaaa gacagg atg 599
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ggc act gct gga aaa gtaagtggaa cattttttgcc tatttcttag gtt att aaa 653
Gly Thr Ala Gly Lys                                     Val Ile Lys
                5

tgc aaa gca gct gtg ctt tgg gag cag aag caa ccc ttc tcc att gag 701
Cys Lys Ala Ala Val Leu Trp Glu Gln Lys Gln Pro Phe Ser Ile Glu
 10                 15                  20                  25

gaa ata gaa gtt gcc cca cca aag act aaa gaa gtt cgc att aag     746
Glu Ile Glu Val Ala Pro Pro Lys Thr Lys Glu Val Arg Ile Lys
                30                  35                  40

gtaagcgtga gcccttgtct ttgaacacag att ttg gcc aca gga atc tgt cgc 800
                               Ile Leu Ala Thr Gly Ile Cys Arg
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aca gat gac cat gtg ata aaa gga aca atg gtg tcc aag ttt cca gtg    848
Thr Asp Asp His Val Ile Lys Gly Thr Met Val Ser Lys Phe Pro Val
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att gtg gga cat gag gca act ggg att gta gag agc att gga gaa gga    896
Ile Val Gly His Glu Ala Thr Gly Ile Val Glu Ser Ile Gly Glu Gly
 65                  70                  75                  80

gtg act aca gtg aaa cca g gtatatgcag gtgtcatttt tttcctgtag gt gac 950
Val Thr Thr Val Lys Pro                                     Gly Asp
                85

aaa gtc atc cct ctc ttt ctg cca caa tgt aga gaa tgc aat gct tgt    998
Lys Val Ile Pro Leu Phe Leu Pro Gln Cys Arg Glu Cys Asn Ala Cys
    90                  95                  100

cgc aac cca gat ggc aac ctt tgc att agg agc ga gtaggtttca          1043
Arg Asn Pro Asp Gly Asn Leu Cys Ile Arg Ser Asp
105                 110                 115

gtcattgatg tatcaaacag t att act ggt cgt gga gta ctg gct gat ggc    1094
                        Ile Thr Gly Arg Gly Val Leu Ala Asp Gly
                                     120                 125

acc acc aga ttt aca tgc aag ggc aaa cca gtc cac cac ttc atg aac    1142
Thr Thr Arg Phe Thr Cys Lys Gly Lys Pro Val His His Phe Met Asn
            130                 135                 140

acc agt aca ttt acc gag tac aca gtg gtg gat gaa tct tct gtt gct    1190
Thr Ser Thr Phe Thr Glu Tyr Thr Val Val Asp Glu Ser Ser Val Ala
            145                 150                 155

aag att gat gat gca gct cct cct gag aaa gtc tgt tta att ggc tgt    1238
Lys Ile Asp Asp Ala Ala Pro Pro Glu Lys Val Cys Leu Ile Gly Cys
    160                 165                 170

ggg ttt tcc act gga tat ggc gct gct gtt aaa act ggc aag            1280
Gly Phe Ser Thr Gly Tyr Gly Ala Ala Val Lys Thr Gly Lys
175                 180                 185

gtaagaaaca gggtacattc ctctccacag gtc aaa cct ggt tcc act tgc gtc   1334
                                   Val Lys Pro Gly Ser Thr Cys Val
                                       190                 195

gtc ttt ggc ctg gga gga gtt ggc ctg tca gtc atc atg ggc tgt aag    1382
Val Phe Gly Leu Gly Gly Val Gly Leu Ser Val Ile Met Gly Cys Lys
            200                 205                 210

tca gct ggt gca tct agg atc att ggg att gac ctc aac aaa gac aaa    1430
Ser Ala Gly Ala Ser Arg Ile Ile Gly Ile Asp Leu Asn Lys Asp Lys
            215                 220                 225

ttt gag aag gcc atg gct gta ggt gcc act gag tgt atc agt ccc aag    1478
Phe Glu Lys Ala Met Ala Val Gly Ala Thr Glu Cys Ile Ser Pro Lys
    230                 235                 240
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gac tct acc aaa ccc atc agt gag gtg ctg tca gaa atg aca ggc aac    1526
Asp Ser Thr Lys Pro Ile Ser Glu Val Leu Ser Glu Met Thr Gly Asn
245             250             255             260

aac gtg gga tac acc ttt gaa gtt att ggg cat ctt gaa acc atg        1571
Asn Val Gly Tyr Thr Phe Glu Val Ile Gly His Leu Glu Thr Met
                265             270             275

gtaagacccc aaaatccgtt ttaaactcag att gat gcc ctg gca tcc tgc cac   1625
                                     Ile Asp Ala Leu Ala Ser Cys His
                                                         280

atg aac tat ggg acc agc gtg gtt gta gga gtt cct cca tca gcc aag    1673
Met Asn Tyr Gly Thr Ser Val Val Val Gly Val Pro Pro Ser Ala Lys
    285             290             295

atg ctc acc tat gac ccg atg ttg ctc ttc act gga cgc aca tgg aag    1721
Met Leu Thr Tyr Asp Pro Met Leu Leu Phe Thr Gly Arg Thr Trp Lys
300             305             310             315

gga tgt gtc ttt gga g gtcaggaaag caaagtgtgc ttatttgcag gt ttg aaa  1775
Gly Cys Val Phe Gly                                     Gly Leu Lys
                320

agc aga gat gat gtc cca aaa cta gtg act gag ttc ctg gca aag aaa    1823
Ser Arg Asp Asp Val Pro Lys Leu Val Thr Glu Phe Leu Ala Lys Lys
    325             330             335

ttt gac ctg gac cag ttg ata act cat gtt tta cca ttt aaa aaa atc    1871
Phe Asp Leu Asp Gln Leu Ile Thr His Val Leu Pro Phe Lys Lys Ile
340             345             350             355

agt gaa gga ttt gag ctg ctc aat tca gga caa ag gtaactgttt         1916
Ser Glu Gly Phe Glu Leu Leu Asn Ser Gly Gln Ser
                360             365

cttatcattt tacatttcag c att cga acg gtc ctg acg ttt tgagatccaa     1968
                        Ile Arg Thr Val Leu Thr Phe
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agtggcagga ggtctgtgtt gtcatggtga actggagttt ctcttgtgag agttccc      2025
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Lys Thr Lys Glu Val Arg Ile Lys Ile Leu Ala Thr Gly Ile Cys Arg
        35              40              45
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Thr Asp Asp His Val Ile Lys Gly Thr Met Val Ser Lys Phe Pro Val
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Ile Val Gly His Glu Ala Thr Gly Ile Val Glu Ser Ile Gly Glu Gly
 65   70   75   80

Val Thr Thr Val Lys Pro Gly Asp Lys Val Ile Pro Leu Phe Leu Pro
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Gln Cys Arg Glu Cys Asn Ala Cys Arg Asn Pro Asp Gly Asn Leu Cys
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Ile Arg Ser Asp Ile Thr Gly Arg Gly Val Leu Ala Asp Gly Thr Thr
      115   120   125

Arg Phe Thr Cys Lys Gly Lys Pro Val His His Phe Met Asn Thr Ser
   130   135   140

Thr Phe Thr Glu Tyr Thr Val Val Asp Glu Ser Ser Val Ala Lys Ile
145   150   155   160

Asp Asp Ala Ala Pro Pro Glu Lys Val Cys Leu Ile Gly Cys Gly Phe
        165   170   175

Ser Thr Gly Tyr Gly Ala Ala Val Lys Thr Gly Lys Val Lys Pro Gly
        180   185   190

Ser Thr Cys Val Val Phe Gly Leu Gly Gly Val Gly Leu Ser Val Ile
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Met Gly Cys Lys Ser Ala Gly Ala Ser Arg Ile Ile Gly Ile Asp Leu
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Asn Lys Asp Lys Phe Glu Lys Ala Met Ala Val Gly Ala Thr Glu Cys
225   230   235   240

Ile Ser Pro Lys Asp Ser Thr Lys Pro Ile Ser Glu Val Leu Ser Glu
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Glu Thr Met Ile Asp Ala Leu Ala Ser Cys His Met Asn Tyr Gly Thr
      275   280   285

Ser Val Val Val Gly Val Pro Pro Ser Ala Lys Met Leu Thr Tyr Asp
      290   295   300

Pro Met Leu Leu Phe Thr Gly Arg Thr Trp Lys Gly Cys Val Phe Gly
305   310   315   320

Gly Leu Lys Ser Arg Asp Asp Val Pro Lys Leu Val Thr Glu Phe Leu
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Ala Lys Lys Phe Asp Leu Asp Gln Leu Ile Thr His Val Leu Pro Phe
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Lys Lys Ile Ser Glu Gly Phe Glu Leu Leu Asn Ser Gly Gln Ser Ile
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Arg Thr Val Leu Thr Phe
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accacatcaa gtctttgcag aatgaagtag agcattaaga agtagagatg tacacacgca 180
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gaaaacttaa aatattatat atgctcttct gttcatattt atactagtca gggagtctgt 180
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ggagatgctt cccatgtttg gagtattaat tcctttactg gctcttatat attgttaagg 480
atctggttgt actcgatgtg aaattaatga gttcattatc c 521

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gatgaccatg tgataaaagg aacaatggtg tccaagtttc cagtgattgt gggacatgag 180

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gcaactggga ttgtagagag cattggagaa ggagtgacta cagtgaaacc aggtatatgc 240
aggtgtcaaa ccacaagttt gaaataatta ggctttgatt agcctatcaa aggaaatagc 300
acacactagg aattattaga gggatcc                                     327
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<212> DNA
<213> Homo sapiens

<400> 13
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cagcatctta tatcatgatt tttttcctgt aggtgacaaa gtcatccctc tctttctgcc 180
acaatgtaga gaatgcaatg cttgtcgcaa cccagatggc aacctttgca ttaggagcga 240
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ctcctcctga gaaagtctgt ttaattggct gtgggttttc cactggatat ggcgctgctg 540
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tcgtctttgg cctgggagga gttggcctgt cagtcatcat gggctgtaag tcagctggtg 180
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gtgccactga gtgtatcagt cccaaggact ctaccaaacc catcagtgag gtgctgtcag 300
aaatgacagg caacaacgtg ggatacacct ttgaagttat tgggcatctt gaaaccatgg 360
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<212> DNA
<213> Homo sapiens

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ctggatgggg agtgatggct ttcactctgg tgcttggcaa gtgggagaag cctgtttcct 240
caggcctttc ttccaagaat gagtatgaag tgatct                           276
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<213> Homo sapiens

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agatgatgtc ccaaaactag tgactgagtt cctggcaaag aaatttgacc tggaccagtt 180
gataactcat gttttaccat ttaaaaaaat cagtgaagga tttgagctgc tcaattcagg 240
acaaaggtaa ctgtttctta tgatga                                     266
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<213> Homo sapiens
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tcagcattcg aacggtcctg acgttttgag atccaaagtg gcaggaggtc tgtgttgtca 120
tggtgaactg gagtttctct tgtgagagtt ccc                             153
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<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Synthetic
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<220>
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<210> 23
<211> 25
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<213> Artificial Sequence

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<210> 24
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<210> 29
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<220>
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<210> 30
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<210> 35
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<400> 35
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<210> 36
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<400> 36
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<210> 37
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<212> DNA
<213> Homo sapiens

<400> 37
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<210> 38
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<400> 38
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<210> 39
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